RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/755,190_
Source: _1FWO_
Date Processed by STIC: _11/2/04_

ENTERED

IFWO

```
 3 <110> APPLICANT: Nikolics, Karoly
 4        McFarland, Keith C.
 5        Segaloff, Deborah L.
 6        Seeburg, Peter H.
 8 <120> TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
10 <130> FILE REFERENCE: P0576P1C3
12 <140> CURRENT APPLICATION NUMBER: US 10/755,190
13 <141> CURRENT FILING DATE: 2004-01-09
15 <150> PRIOR APPLICATION NUMBER: US 09/877,804
16 <151> PRIOR FILING DATE: 2001-06-07
18 <150> PRIOR APPLICATION NUMBER: US 08/207,814
19 <151> PRIOR FILING DATE: 1994-03-07
21 <150> PRIOR APPLICATION NUMBER: US 07/781,153
22 <151> PRIOR FILING DATE: 1991-10-31
24 <150> PRIOR APPLICATION NUMBER: PCT/US90/02488
25 <151> PRIOR FILING DATE: 1990-05-04
27 <150> PRIOR APPLICATION NUMBER: US 07/347,683
28 <151> PRIOR FILING DATE: 1989-05-05
30 <160> NUMBER OF SEQ ID NOS: 22
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 2902
34 <212> TYPE: DNA
35 <213> ORGANISM: Rattus
37 <400> SEQUENCE: 1
38  atactggctc aacctcggga gctcacactc aggctggcgg gcc atg 46
39                                                  Met
40                                                  1
42  ggg cgg cga gtc cca gct ctg aga cag ctg ctg gtg ctg 85
43  Gly Arg Arg Val Pro Ala Leu Arg Gln Leu Leu Val Leu
44              5                   10
46  gca gtg ctg ctg ctg aag cct tca cag ctg cag tcc cga 124
47  Ala Val Leu Leu Leu Lys Pro Ser Gln Leu Gln Ser Arg
48   15                  20                  25
50  gag ctg tca ggg tcg cgc tgc ccc gag ccc tgc gac tgc 163
51  Glu Leu Ser Gly Ser Arg Cys Pro Glu Pro Cys Asp Cys
52          30                  35                  40
54  gca ccg gat ggc gcc ctg cgc tgt cct ggc cct cga gcc 202
55  Ala Pro Asp Gly Ala Leu Arg Cys Pro Gly Pro Arg Ala
56                  45                  50
58  ggc ctc gcc aga cta tct ctc acc tat ctc cct gtc aaa 241
59  Gly Leu Ala Arg Leu Ser Leu Thr Tyr Leu Pro Val Lys
60      55                  60                  65
62  gta att cca tca caa gct ttc agg gga ctt aat gag gtc 280
```

```
63   Val Ile Pro Ser Gln Ala Phe Arg Gly Leu Asn Glu Val
64               70                      75
66   gta aaa att gaa atc tct cag agt gat tcc ctg gaa agg 319
67   Val Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg
68    80                  85                  90
70   ata gaa gct aat gcc ttt gac aac ctc ctc aat ttg tct 358
71   Ile Glu Ala Asn Ala Phe Asp Asn Leu Leu Asn Leu Ser
72            95                  100                 105
74   gaa cta ctg atc cag aac acc aaa aac ctg cta tac att 397
75   Glu Leu Leu Ile Gln Asn Thr Lys Asn Leu Leu Tyr Ile
76                  110                 115
78   gaa cct ggt gct ttt aca aac ctc cct cgg tta aaa tac 436
79   Glu Pro Gly Ala Phe Thr Asn Leu Pro Arg Leu Lys Tyr
80        120                 125                 130
82   ctg agc atc tgt aac aca ggc atc cga acc ctt cca gat 475
83   Leu Ser Ile Cys Asn Thr Gly Ile Arg Thr Leu Pro Asp
84                  135                 140
86   gtt acg aag atc tcc tcc tct gaa ttt aat ttc att ctg 514
87   Val Thr Lys Ile Ser Ser Ser Glu Phe Asn Phe Ile Leu
88   145                 150                 155
90   gaa atc tgt gat aac tta cac ata acc acc ata ccc ggg 553
91   Glu Ile Cys Asp Asn Leu His Ile Thr Thr Ile Pro Gly
92            160                 165                 170
94   aat gct ttc caa ggg atg aat aac gag tct gtc aca cta 592
95   Asn Ala Phe Gln Gly Met Asn Asn Glu Ser Val Thr Leu
96                  175                 180
98   aaa ctg tat gga aat gga ttt gaa gaa gta caa agc cat 631
99   Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser His
100      185                 190                 195
102  gca ttc aat ggg acg act cta atc tcg ctg gag cta aaa 670
103  Ala Phe Asn Gly Thr Thr Leu Ile Ser Leu Glu Leu Lys
104                  200                 205
106  gaa aac atc tac ctg gag aag atg cac agt gga gcc ttc 709
107  Glu Asn Ile Tyr Leu Glu Lys Met His Ser Gly Ala Phe
108  210                 215                 220
110  cag ggg gcc acg ggg ccc agc atc ctg gat att tct tcc 748
111  Gln Gly Ala Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser
112          225                 230                 235
114  acc aaa ttg cag gcc ctg ccg agc cac ggg ctg gag tcc 787
115  Thr Lys Leu Gln Ala Leu Pro Ser His Gly Leu Glu Ser
116                  240                 245
118  att cag acg ctc atc gcc ctg tct tcc tac tca ctg aaa 826
119  Ile Gln Thr Leu Ile Ala Leu Ser Ser Tyr Ser Leu Lys
120      250                 255                 260
122  aca ctg ccc tcc aaa gaa aaa ttc acg agc ctc ctg gtc 865
123  Thr Leu Pro Ser Lys Glu Lys Phe Thr Ser Leu Leu Val
124          265                 270
126  gcc acg ctg acc tac ccc agc cac tgc tgc gcc ttc agg 904
127  Ala Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg
```

```
128  275                    280                    285
130  aat ttg ccg aag aaa gaa cag aat ttt tca ttt tcc att 943
131  Asn Leu Pro Lys Lys Glu Gln Asn Phe Ser Phe Ser Ile
132           290                    295                    300
134  ttt gaa aac ttc tcc aaa caa tgc gaa agc aca gtt aga 982
135  Phe Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg
136                    305                    310
138  aaa gca gat aac gag acg ctt tat tcc gcc atc ttt gag 1021
139  Lys Ala Asp Asn Glu Thr Leu Tyr Ser Ala Ile Phe Glu
140      315                    320                    325
142  gag aat gaa ctc agt ggc tgg gat tat gat tat ggc ttc 1060
143  Glu Asn Glu Leu Ser Gly Trp Asp Tyr Asp Tyr Gly Phe
144           330                    335
146  tgt tca ccc aag aca ctc caa tgt gct cca gaa cca gat 1099
147  Cys Ser Pro Lys Thr Leu Gln Cys Ala Pro Glu Pro Asp
148  340                    345                    350
150  gct ttc aac ccc tgt gaa gat att atg ggc tat gcc ttc 1138
151  Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Ala Phe
152           355                    360                    365
154  ctt agg gtc ctg att tgg ctg att aat ata cta gcc atc 1177
155  Leu Arg Val Leu Ile Trp Leu Ile Asn Ile Leu Ala Ile
156                    370                    375
158  ttt ggc aac ctg aca gtc ctc ttt gtt ctc ctg acc agt 1216
159  Phe Gly Asn Leu Thr Val Leu Phe Val Leu Leu Thr Ser
160      380                    385                    390
162  cgt tat aaa ctg aca gtg ccc cgc ttc ctc atg tgt aat 1255
163  Arg Tyr Lys Leu Thr Val Pro Arg Phe Leu Met Cys Asn
164           395                    400
166  ctc tcc ttt gca gac ttt tgc atg ggg ctc tac ctg ctg 1294
167  Leu Ser Phe Ala Asp Phe Cys Met Gly Leu Tyr Leu Leu
168  405                    410                    415
170  ctc att gcc tcc gtg gac tcc caa aca aaa ggc cag tac 1333
171  Leu Ile Ala Ser Val Asp Ser Gln Thr Lys Gly Gln Tyr
172           420                    425                    430
174  tat aac cac gcc ata gac tgg cag aca ggg agt ggc tgc 1372
175  Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys
176                    435                    440
178  ggt gca gct ggc ttc ttt act gtg ttt gcc agt gaa ctc 1411
179  Gly Ala Ala Gly Phe Phe Thr Val Phe Ala Ser Glu Leu
180      445                    450                    455
182  tct gtc tac acc ctg acg gtt atc acc ctg gaa agg tgg 1450
183  Ser Val Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp
184           460                    465
186  cac acc atc acc tat gct gta cag cta gac caa aag cta 1489
187  His Thr Ile Thr Tyr Ala Val Gln Leu Asp Gln Lys Leu
188  470                    475                    480
190  aga ctg agg cat gcc atc cca att atg ctc gga gga tgg 1528
191  Arg Leu Arg His Ala Ile Pro Ile Met Leu Gly Gly Trp
192           485                    490                    495
```

Input Set : **A:\P0576P1C3.txt**
Output Set: **N:\CRF4\11022004\J755190.raw**

```
194  ctc ttt tct acg ctg atc gcc acg atg ccc ctt gtg ggt 1567
195  Leu Phe Ser Thr Leu Ile Ala Thr Met Pro Leu Val Gly
196              500              505
198  atc agc aat tac atg aag gtc agc atc tgc ctc ccc atg 1606
199  Ile Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met
200      510              515              520
202  gat gtg gaa tcc act ctg tcc caa gtc tac ata tta tcc 1645
203  Asp Val Glu Ser Thr Leu Ser Gln Val Tyr Ile Leu Ser
204              525              530
206  atc tta atc ctc aac gtg gtg gcc ttc gtc gtc atc tgt 1684
207  Ile Leu Ile Leu Asn Val Val Ala Phe Val Val Ile Cys
208  535              540              545
210  gct tgc tac att agg atc tac ttt gca gtt caa aat cca 1723
211  Ala Cys Tyr Ile Arg Ile Tyr Phe Ala Val Gln Asn Pro
212      550              555              560
214  gag ctg aca gct cct aac aag gac aca aaa att gct aag 1762
215  Glu Leu Thr Ala Pro Asn Lys Asp Thr Lys Ile Ala Lys
216              565              570
218  aag atg gcc atc ctc atc ttc aca gac ttc acg tgc atg 1801
219  Lys Met Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met
220      575              580              585
222  gcg ccc atc tct ttc ttt gcc atc tcg gct gcc ttc aaa 1840
223  Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys
224              590              595
226  gtg ccc ctt atc act gtc acc aac tcg aaa atc tta ctg 1879
227  Val Pro Leu Ile Thr Val Thr Asn Ser Lys Ile Leu Leu
228  600              605              610
230  gtc ctt ttt tat cct gtc aat tct tgt gcc aat cca ttt 1918
231  Val Leu Phe Tyr Pro Val Asn Ser Cys Ala Asn Pro Phe
232      615              620              625
234  ctg tat gcg atc ttc acg aag gcg ttt cag aga gat ttc 1957
235  Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Phe
236              630              635
238  ctt ctg ctg ctg agc cga ttc ggc tgc tgt aaa cgc cgg 1996
239  Leu Leu Leu Leu Ser Arg Phe Gly Cys Cys Lys Arg Arg
240      640              645              650
242  gcg gag ctt tac aga agg aag gaa ttt tct gca tat act 2035
243  Ala Glu Leu Tyr Arg Arg Lys Glu Phe Ser Ala Tyr Thr
244              655              660
246  tcc aac tgc aaa aat ggc ttc cca gga gca agt aag ccg 2074
247  Ser Asn Cys Lys Asn Gly Phe Pro Gly Ala Ser Lys Pro
248  665              670              675
250  tcc cag gct acc ctg aag ttg tcc aca gtg cac tgt caa 2113
251  Ser Gln Ala Thr Leu Lys Leu Ser Thr Val His Cys Gln
252      680              685              690
254  cag ccc ata cca ccg aga gcg tta act cac tagcatt 2150
255  Gln Pro Ile Pro Pro Arg Ala Leu Thr His
256              695              700
258  acaaaattgt gcctaaatat gttttttaaa aagtgtttta gaaaaatatt 2200
```

```
260   tatccttagg cacttcagga gaattgtacc tgcttcagag gacggcctat 2250
262   aacacttggt cacataagtt tcaggaaggt ttagaaattt ttatagtaat 2300
264   ttaggcataa taatttttttg ttgaatctaa tactaaggaa atctaagttg 2350
266   tcattttttca cgtctctgac atttttcatt tcaatcttgt gatttacatt 2400
268   gtaatctcca aatatattac ttcatagcag attgaaaatt taaactggtc 2450
270   tttgtcctca gatagtttga taaatatatt caagagatgc actgtgcagt 2500
272   gtgactgcta gccttgcatg gtaaatagaa gtttcttagc catattccaa 2550
274   gtgcttcaca tgtcacacta ggaggcacag atgcaaactg tttacatcag 2600
276   tgaattctat tagccagctc tattctagag acttctattt cccattgaca 2650
278   ctctgcttaa ctttccatct gaaggcacat gctgcatatt tgtttggctt 2700
280   acagatcatg agtacctcat ggccaggagc ccatctcagc ccatcttgtt 2750
282   cctcgtctat ctcaggatct tggaaatgct acacagcaag catgcctagc 2800
284   cagttaaact ccctaaatct acacaggaaa atatttctac caccttagca 2850
286   tattgttttc gatgattaca tgctttctgt attttgccct cctcctagta 2900
288   tc 2902
290   <210> SEQ ID NO: 2
291   <211> LENGTH: 700
292   <212> TYPE: PRT
293   <213> ORGANISM: Artificial Sequence
295   <220> FEATURE:
296   <223> OTHER INFORMATION: deduced sequence
298   <400> SEQUENCE: 2
299   Met Gly Arg Arg Val Pro Ala Leu Arg Gln Leu Leu Val Leu Ala
300    1               5                   10                  15
302   Val Leu Leu Leu Lys Pro Ser Gln Leu Gln Ser Arg Glu Leu Ser
303                   20                  25                  30
305   Gly Ser Arg Cys Pro Glu Pro Cys Asp Cys Ala Pro Asp Gly Ala
306                   35                  40                  45
308   Leu Arg Cys Pro Gly Pro Arg Ala Gly Leu Ala Arg Leu Ser Leu
309                   50                  55                  60
311   Thr Tyr Leu Pro Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly
312                   65                  70                  75
314   Leu Asn Glu Val Val Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu
315                   80                  85                  90
317   Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn Leu Leu Asn Leu Ser
318                   95                  100                 105
320   Glu Leu Leu Ile Gln Asn Thr Lys Asn Leu Leu Tyr Ile Glu Pro
321                   110                 115                 120
323   Gly Ala Phe Thr Asn Leu Pro Arg Leu Lys Tyr Leu Ser Ile Cys
324                   125                 130                 135
326   Asn Thr Gly Ile Arg Thr Leu Pro Asp Val Thr Lys Ile Ser Ser
327                   140                 145                 150
329   Ser Glu Phe Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu His Ile
330                   155                 160                 165
332   Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly Met Asn Asn Glu Ser
333                   170                 175                 180
335   Val Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser
336                   185                 190                 195
338   His Ala Phe Asn Gly Thr Thr Leu Ile Ser Leu Glu Leu Lys Glu
```

VERIFICATION SUMMARY   DATE: 11/02/2004
PATENT APPLICATION: **US/10/755,190**   TIME: 13:32:48

Input Set : **A:\P0576P1C3.txt**
Output Set: **N:\CRF4\11022004\J755190.raw**